

SEQUENCE LISTING

<110> Duvick, Jonathan P.
 Gilliam, Jacob T.
 Maddox, Joyce R.
 Crasta, Oswald R.
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 0875C

<150> US 60/092,936

<151> 1998-07-15

<150> US 09/352,168

<151> 1999-07-12

<160> 33

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 372

<212> DNA

<213> *Exophiala spinifera*.

<220>

<221> misc_feature

<222> (346)...(346)

<223> n = A,T,C or G

<400> 1

gggccccggc gttctcgtag gctgcgcgga gttgggtcca gacagacttt tgtcgtacct	60
gcttggaactg ttgggaccac ttcggtcccg ggtctccgac catgaaacag gtaatggacc	120
attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggggtca cagctcgatt	180
ggaggacgcc cgagaagcct tgttcgcgcc accacggctt gtcccatacg aagactatct	240
tgctatagta gccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg	300
gtgaaaatgt caagtgggga tacaagggtg tcggtaacga aaccancacc ttttgcttc	360
ggaacacggc gc	372

<210> 2

<211> 182

<212> DNA

<213> *Exophiala spinifera*.

<400> 2

gaattttccg ccaatgcttg cttctcggcg ggaagaggtg gtgaaaatgt caagtgggga	60
tacaagggtg tcggtaacga aaccaccacc ttttgcttc ggaacacggc gcccgaggcc	120
gatcgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc	180
ac	182

<210> 3

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 3

tggtttcgtt accgacaacc ttgtatccc

29

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 5' RACE, N21968

<400> 4

gagttggtcc cagacagact tttgtcgt

28

<210> 5

<211> 1389

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> CDS

<222> (1) ... (1386)

<400> 5

gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
1 5 10 15

48

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
20 25 30

96

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35 40 45

144

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

192

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

240

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

288

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

336

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

384

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 135 140

432

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145 150 155 160	480
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly 165 170 175	528
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180 185 190	576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195 200 205	624
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met 210 215 220	672
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala 225 230 235 240	720
gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly 245 250 255	768
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu 260 265 270	816
tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala 275 280 285	864
ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val 290 295 300	912
tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln 305 310 315 320	960
tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val 325 330 335	1008
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg 340 345 350	1056
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp 355 360 365	1104
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro 370 375 380	1152
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly 385 390 395 400	1200

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: a control group (n = 10) and an experimental group (n = 10). The control group received a placebo (PLA) and the experimental group received a 10% w/v solution of the active ingredient (10% w/v). The subjects were divided into two groups: a control group (n = 10) and an experimental group (n = 10). The control group received a placebo (PLA) and the experimental group received a 10% w/v solution of the active ingredient (10% w/v). The subjects were divided into two groups: a control group (n = 10) and an experimental group (n = 10). The control group received a placebo (PLA) and the experimental group received a 10% w/v solution of the active ingredient (10% w/v).

<400> 6															
Asp 1	Asn	Val	Ala	Asp 5	Val	Val	Val	Val	Gly 10	Ala	Gly	Leu	Ser	Gly 15	Leu
Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu
			20				25				30				
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
			35				40				45				
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
			50				55				60				
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
65				70				75				80			
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
			85				90				95				
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
			100				105				110				
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile
			115				120				125				
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
			130				135				140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
145				150				155				160			
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
			165				170				175				
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
			180				185				190				
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
			195				200				205				
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met
			210				215				220				
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala
225				230				235				240			
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly
			245				250				255				
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu
			260				265				270				
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala
			275				280				285				

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 435 440 445
 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 7
 <211> 1442
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(646)
 <221> intron
 <222> (647)...(699)

<221> CDS
 <222> (700)...(1439)

<400> 7

gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg	48
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu	
1 5 10 15	
gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
ggt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgcgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	
210 215	
tcgtttctca gtggtcattc cag gt atg cag tcg att tgc cat gcc atg tca	728
Gly Met Gln Ser Ile Cys His Ala Met Ser	
220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
290 295 300 305	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg	1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	1064

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
 325 330 335

cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag 1112
 Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
 340 345 350

tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa 1160
 Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
 355 360 365

ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc 1208
 Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
 370 375 380 385

aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct 1256
 Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
 390 395 400

ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg 1304
 Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
 405 410 415

ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct 1352
 Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
 420 425 430

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga 1400
 Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
 435 440 445

ggg gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1442
 Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 8
 <211> 462
 <212> PRT
 <213> Exophiala spinifera

<400> 8

Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
 1 5 10 15
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365
 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380
 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 420 425 430
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 435 440 445
 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 9

<211> 458

<212> PRT

<213> *Exophiala spinifera*

<400> 9

Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
 1 5 10 15
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg


```

      130              135              140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145              150              155              160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
      165              170              175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
      180              185              190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
      195              200              205
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
      210              215              220
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
225              230              235              240
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
      245              250              255
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
      260              265              270
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
      275              280              285
Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys
      290              295              300
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
305              310              315              320
Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
      325              330              335
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
      340              345              350
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
      355              360              365
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
      370              375              380
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
385              390              395              400
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
      405              410              415
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
      420              425              430
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu
      435              440              445
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
450              455

```

```

<210> 10
<211> 1392
<212> DNA
<213> Exophiala spinifera

```

```

<220>
<221> CDS
<222> (1)...(1389)

<221> misc_feature
<222> (1)...(3)
<223> Extra lysine in K:trAPAO

```

```

      <400> 10
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
  1              5              10              15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val

```

20	25	30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg			144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
35	40	45	
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat			192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg			240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
65	70	75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa			288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag			336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
100	105	110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg			384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag			432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac			480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc			528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc			576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc			624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc			672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg			768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc			816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	
tag	1392

<210> 11

<211> 463

<212> PRT

<213> Exophiala spinifera

<220>

<223> Extra lysine in the polypeptide sequence of
K:trAPAO, 463 aa.

<400> 11

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
1				5					10				15		

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

```

<220>
<223> Primer sequence designed for cloning DNA into
expression vectors, N23256

<400> 12
ggggaattca aagacaacgt tgcggacgtg gtag 34

<210> 13
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence designed for cloning DNA into
expression vectors, N23259

<400> 13
ggggcggcgc cctatgctgc tggcaccagg ctag 34

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
tggtttcggt accgacaacc ttgtatccc 29

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide for 5' race, N21968

<400> 15
gagttggtcc cagacagact tttgtcgt 28

<210> 16
<211> 1673
<212> DNA
<213> Exophiala spinifera

<220>
<221> sig_peptide
<222> (1)...(267)
<223> yeast alpha mating factor secretion signal.

<221> CDS
<222> (1)...(1662)

<400> 16
atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc 48
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
-85 -80 -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
-70 -65 -60

```

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 -55 -50 -45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -40 -35 -30

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta 240
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -25 -20 -15 -10

tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg 288
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 -5 1 5

gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc 336
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
 10 15 20

aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat 384
 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
 25 30 35

cgt gta ggg gga aag act ctg agc gta caa tcc ggt ccc ggc agg acg 432
 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
 40 45 50 55

act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc 480
 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
 60 65 70

gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag 528
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
 75 80 85

agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act 576
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
 90 95 100

aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca 624
 Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
 105 110 115

ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc 672
 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
 120 125 130 135

ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg 720
 Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
 140 145 150

agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc 768
 Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
 155 160 165

ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac 816
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
 170 175 180

gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt 864

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	
185	190 195
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga	912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	
200	205 210 215
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt	960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu	
	220 225 230
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln	
	235 240 245
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga	1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg	
	250 255 260
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg	1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu	
	265 270 275
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat	1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn	
	280 285 290 295
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg	1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro	
	300 305 310
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac	1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp	
	315 320 325
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg	1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp	
	330 335 340
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa	1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln	
	345 350 355
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca	1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala	
	360 365 370 375
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc	1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu	
	380 385 390
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
	395 400 405
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg	1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr	
	410 415 420
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg	1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp	
	425 430 435

aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca 1632
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
 440 445 450 455

gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c 1673
 Glu Val Val Ala Ser Leu Val Pro Ala Ala
 460 465

<210> 17
 <211> 554
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> SIGNAL
 <222> (1)...(89)
 <223> yeast alpha mating factor secretion signal.

<400> 17
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
 -70 -65 -60
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 -55 -50 -45
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -40 -35 -30
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -25 -20 -15 -10
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 -5 1 5
 Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
 10 15 20
 Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
 25 30 35
 Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
 40 45 50 55
 Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
 60 65 70
 Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
 75 80 85
 Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
 90 95 100
 Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
 105 110 115
 Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
 120 125 130 135
 Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
 140 145 150
 Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
 155 160 165
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
 170 175 180
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
 185 190 195
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
 200 205 210 215
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
 220 225 230
 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln


```

                235                240                245
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
                250                255                260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
                265                270                275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
280                285                290                295
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
                300                305                310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
                315                320                325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
                330                335                340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
                345                350                355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
360                365                370                375
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
                380                385                390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
                395                400                405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
                410                415                420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
                425                430                435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
440                445                450                455
Glu Val Val Ala Ser Leu Val Pro Ala Ala
                460                465

```

<210> 18

<211> 2079

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1) ... (2076)

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
- 687, gst fusion + polylinker; 688-2076,
K:trAPAO; 2077-2079, stop codon. For bacterial
expression.

<221> misc_feature

<222> (1) ... (687)

<223> gst fusion + polylinker

<221> misc_feature

<222> (688) ... (2076)

<223> K:trAPAO

<221> misc_feature

<222> (688) ... (690)

<223> Extra lysine

<400> 18

```

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1                5                10                15

```

48

```

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg

```

96

Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu		
		20						25					30				
tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144	
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu		
		35					40					45					
ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	gtt	aaa	192	
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys		
	50					55					60						
tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240	
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn		
	65				70					75					80		
atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288	
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu		
				85				90						95			
gga	gcg	gtt	ttg	gat	att	aga	tac	ggt	gtt	tcg	aga	att	gca	tat	agt	336	
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser		
			100					105					110				
aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384	
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu		
		115					120					125					
atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432	
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn		
	130					135					140						
ggt	gat	cat	gta	acc	cat	cct	gac	ttc	atg	ttg	tat	gac	gct	ctt	gat	480	
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp		
	145				150					155				160			
gtt	gtt	tta	tac	atg	gac	cca	atg	tgc	ctg	gat	gcg	ttc	cca	aaa	tta	528	
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu		
				165				170						175			
gtt	tgt	ttt	aaa	aaa	cgt	att	gaa	gct	atc	cca	caa	att	gat	aag	tac	576	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr		
			180				185						190				
ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	goc	624	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala		
		195					200					205					
acg	ttt	ggt	ggt	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	gtt	ccg	cgt	672	
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg		
	210				215						220						
gga	tcc	ccg	gaa	ttc	aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	720	
Gly	Ser	Pro	Glu	Phe	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly		
	225				230					235					240		
gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggt	768	
Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly		
				245				250						255			
ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	816	
Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr		
			260					265					270				

ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285	864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300	912
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305 310 315 320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp 325 330 335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340 345 350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355 360 365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370 375 380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385 390 395 400	1200
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405 410 415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser 420 425 430	1296
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln 435 440 445	1344
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His 450 455 460	1392
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr 465 470 475 480	1440
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val 485 490 495	1488
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu 500 505 510	1536
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584

```

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
    515                                520                                525

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc      1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
    530                                535                                540

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga      1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
    545                                550                                555                                560

gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg      1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
    565                                570                                575

gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga      1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
    580                                585                                590

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg      1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
    595                                600                                605

gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag      1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
    610                                615                                620

cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat      1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
    625                                630                                635                                640

ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat      1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
    645                                650                                655

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg      2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
    660                                665                                670

gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg      2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
    675                                680                                685

gtg cca gca gca tag      2079
Val Pro Ala Ala
    690

```

```

<210> 19
<211> 692
<212> PRT
<213> Unknown

```

```

<220>
<223> GST:K:trAPAO; GST + linker, aa 1-229; K:trAPAO, aa
      230-692

```

```

<400> 19
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1           5           10           15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
      20           25           30

```

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
 225 230 235 240
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
 245 250 255
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
 260 265 270
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
 275 280 285
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
 290 295 300
 Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
 340 345 350
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495
 Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525

```

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
530          535          540
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
545          550          555          560
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
565          570          575
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
580          585          590
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
595          600          605
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
610          615          620
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625          630          635          640
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
645          650          655
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
660          665          670
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
675          680          685
Val Pro Ala Ala
690

```

```

<210> 20
<211> 1464
<212> DNA
<213> Unknown

```

```

<220>
<221> sig_peptide
<222> (1)...(72)
<223> Barley Alpha Amylase signal sequence.

```

```

<221> misc_feature
<222> (73)...(1464)
<223> K:trAPAOcDNA

```

```

<221> CDS
<222> (1)...(1461)

```

```

<223> Nucleotide sequence of K:trAPAO translational
      fusion with barley alpha amylase signal sequence,
      for expression and secretion of the mature trAPAO
      in maize. Nucleotides 1-72, barley alpha amylase
      signal sequence, nucleotides 73-75, added lysine
      residue; nucleotides 76 -1464 , trAPAO cDNA.

```

```

<221> misc_feature
<222> (73)...(75)
<223> Added lysine residue

```

```

<400> 20
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc      48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
      -20          -15          -10

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta      96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
      -5          1          5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag      144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

```

10	15	20	
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly 25 30 35 40			192
gga aag act ctg agc gta caa tcg ggt ccc gcc agg acg act atc aac Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn 45 50 55			240
gac ctc gcc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser 60 65 70			288
aga ttg ttt gaa aga ttt cat ttg gag gcc gag ctc cag agg acg act Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr 75 80 85			336
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro 90 95 100			384
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu 105 110 115 120			432
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp 125 130 135			480
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala 140 145 150			528
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc gcc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala 155 160 165			576
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser 170 175 180			624
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn 185 190 195 200			672
att ttc tcg gac aag aaa gac gcc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr 205 210 215			720
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca gcc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly 220 225 230			768
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser 235 240 245			816
ggc tgt aca gta cga tcg gcc tcg gcc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys 250 255 260			864

```

gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca      912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
265                      270                      275                      280

cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg      960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
                      285                      290                      295

ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc      1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
                      300                      305                      310

gaa caa ggc ttc tcg gcc gtc ctc caa tcg agc tgt gac ccc atc tca      1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
                      315                      320                      325

ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc      1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
                      330                      335                      340

tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag      1152
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
345                      350                      355                      360

cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag      1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
                      365                      370                      375

aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag      1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
                      380                      385                      390

tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg      1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
                      395                      400                      405

ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag      1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
                      410                      415                      420

agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat      1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
425                      430                      435                      440

atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg      1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
                      445                      450                      455

gct agc ctg gtg cca gca gca tag      1464
Ala Ser Leu Val Pro Ala Ala
                      460

```

```

<210> 21
<211> 487
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1) ... (24)

```


<223> K:trAPAO translational fusion with barley alpha
amylase signal sequence, for expression and
secretion of the mature trAPAO in maize.

<400> 21

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
				-20					-15					-10	
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Lys	Asp	Asn	Val	Ala	Asp	Val	Val
			-5					1				5			
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
	10					15					20				
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
25					30					35					40
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
				45					50					55	
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser
			60					65					70		
Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
		75					80					85			
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
	90					95					100				
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
105					110					115					120
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
				125					130					135	
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
			140					145					150		
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
		155					160					165			
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
	170					175						180			
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
185					190					195					200
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
				205					210					215	
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
			220					225					230		
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
		235					240					245			
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys
	250					255					260				
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser
265					270					275					280
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu
				285					290					295	
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg
			300					305					310		
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser
		315				320						325			
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr
	330					335					340				
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys
345					350					355					360
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu
				365					370					375	
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu
			380					385					390		
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly
		395					400					405			
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys
	410					415					420				
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr

[illegible]

```
<220>  
<221> CDS  
<222> (1) ... (1800)
```

<400> 22																
atg	gca	ctt	gca	ccg	agc	tac	atc	aat	ccc	cca	aac	gtc	gcc	tcc	cca	48
Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro	
1				5				10						15		
gca	ggg	tat	tct	cac	gtc	ggc	gta	ggc	cca	gac	gga	ggg	agg	tat	gtg	96
Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val	
		20						25				30				
aca	ata	gct	gga	cag	att	gga	caa	gac	gct	tcg	ggc	gtg	aca	gac	cct	144
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro	
35						40						45				
gcc	tac	gag	aaa	cag	gtt	gcc	caa	gca	ttc	gcc	aat	ctg	cga	gct	tgc	192
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	
50						55						60				
ctt	gct	gca	gtt	gga	gcc	act	tca	aac	gac	gtc	acc	aag	ctc	aat	tac	240
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr	
65				70						75				80		
tac	atc	gtc	gac	tac	gcc	ccg	agc	aaa	ctc	acc	gca	att	gga	gat	ggg	288
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	
				85						90				95		
ctg	aag	gct	acc	ttt	gcc	ctt	gac	agg	ctc	cct	cct	tgc	acg	ctg	gtg	336
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	
		100						105				110				
cca	gtg	tcg	gcc	ttg	tct	tca	cct	gaa	tac	ctc	ttt	gag	gtt	gat	gcc	384
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	
115						120						125				
acg	gcg	ctg	gtg	cog	gga	cac	acg	acc	cca	gac	aac	gtt	gcg	gac	gtg	432
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	
130						135						140				
gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt	ttg	gag	acg	gca	cgc	aaa	gtc	480
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	
145				150						155				160		
cag	gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	528
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	
				165				170						175		
ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	act	atc	576
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	

180	185	190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195 200 205			624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220			672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 225 230 235 240			720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255			768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270			816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285			864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300			912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320			960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335			1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350			1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355 360 365			1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370 375 380			1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385 390 395 400			1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405 410 415			1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420 425 430			1296

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg 1344
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
 435 440 445

 cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc 1392
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460

 tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att 1440
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
 465 470 475 480

 acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc 1488
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495

 aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac 1536
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510

 gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc 1584
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525

 gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540

 ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc 1680
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560

 aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg 1728
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575

 tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt 1776
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590

 gtg gct agc ctg gtg cca gca gca tag 1803
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 23
 <211> 600
 <212> PRT
 <213> *Exophiala spinifera*

<400> 23
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

				85					90				95				
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val		
			100					105					110				
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala		
		115					120					125					
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val		
	130				135						140						
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val		
145					150				155						160		
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val		
			165				170						175				
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile		
		180					185					190					
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val		
	195					200					205						
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr		
	210					215					220						
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala		
225				230					235						240		
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala		
			245					250						255			
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln		
		260					265						270				
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe		
	275					280					285						
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val		
	290					295				300							
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile		
305				310					315					320			
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser		
			325					330					335				
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys		
		340					345					350					
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro		
	355					360					365						
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala		
	370				375						380						
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys		
385				390					395						400		
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe		
			405					410					415				
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile		
		420						425				430					
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp		
	435					440						445					
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		
	450					455					460						
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile		
465				470					475					480			
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser		
			485					490					495				
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr		
		500						505				510					
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile		
	515					520					525						
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr		
	530				535					540							
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe		
545				550					555					560			
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly		
			565					570				575					
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val		

Val Ala Ser Leu Val Pro Ala Ala
 580 585 590
 595 600

<210> 24
 <211> 3003
 <212> DNA
 <213> Unknown

<220>
 <223> Sequence is a barley alpha amylase signal
 sequence: esp1 mat: an artificial spacer sequence
 and K:trAPAO

<221> sig_peptide
 <222> (1)...(72)
 <223> Barley alpha amylase signal sequence

<221> misc_feature
 <222> (73)...(1575)
 <223> esp1 mat

<221> misc_feature
 <222> (1576)...(1611)
 <223> spacer sequence

<221> misc_feature
 <222> (1612)...(3000)
 <223> K:trAPAO

<221> CDS
 <222> (1)...(3000)

<221> misc_feature
 <222> (1612)...(1614)
 <223> Extra lysine

<400> 24
 atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
 -20 -15 -10

ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96
 Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
 -5 1 5

ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144
 Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20

gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
 25 30 35 40

gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
 45 50 55

gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc 288
 Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
 60 65 70

cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag	912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	
265 270 275 280	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
285 290 295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc	1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	
300 305 310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat	1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	

315	320	325	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu 330 335 340			1104
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln 345 350 355 360			1152
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile 365 370 375			1200
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr 380 385 390			1248
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val 395 400 405			1296
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala 410 415 420			1344
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala 425 430 435 440			1392
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln 445 450 455			1440
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val 460 465 470			1488
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg 475 480 485			1536
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly 490 495 500			1584
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val 505 510 515 520			1632
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535			1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550			1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555 560 565			1776

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755 760	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765 770 775	2400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790	2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 795 800 805	2496
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	2544

The following table shows the amino acid sequence of the protein.

810	815	820	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
825	830	835	840
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
	845	850	855
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc			2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
	860	865	870
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac			2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
	875	880	885
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc			2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
	890	895	900
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat			2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
905	910	915	920
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc			2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
	925	930	935
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg			2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
	940	945	950
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt			2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
	955	960	965
gtg gct agc ctg gtg cca gca gca tag			3003
Val Ala Ser Leu Val Pro Ala Ala			
970	975		

<210> 25

<211> 1000

<212> PRT

<213> Unknown

<220>

<221> SIGNAL

<222> (1)...(24)

<400> 25

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
				-20					-15					-10	
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala
			-5				1				5				
Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr
10					15				20						
Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe
25				30				35					40		
Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr

				45					50					55		
Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu	
			60					65					70			
Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly	
		75					80					85				
Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu	
		90				95					100					
Asn	Thr	Asn	Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu	
105					110					115					120	
Tyr	Gly	Trp	Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala	
			125						130					135		
Asn	Gln	Asp	Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	
			140					145					150			
Gly	Phe	Pro	Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly	
		155					160				165					
Phe	Leu	Asp	Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala	
		170				175					180					
Ala	Phe	Gly	Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala	
185					190					195					200	
Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro	
			205						210					215		
Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe	
			220					225					230			
Pro	Lys	Gly	Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu	
		235					240					245				
Asn	Cys	Thr	Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp	
		250				255					260					
Leu	Ala	Thr	Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu	
265					270					275					280	
Tyr	Thr	Leu	Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg	
			285						290						295	
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala	
			300					305					310			
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr	
		315					320					325				
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu	
		330				335					340					
Gly	Ala	Tyr	Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln	
345					350					355					360	
Ile	Ala	Ala	Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile	
			365						370					375		
Val	Ala	Gln	Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr	
			380													

<210>	26
<211>	2976
<212>	DNA
<213>	Unknown

1

<223> Barley alpha amylase signal sequence: BEST1
mature: artificial spacer: and K:trAPAO. For
plant expression.

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence.

<221> mat_peptide
<222> (73)...(1545)
<223> BEST1 mature

<221> misc_feature
<222> (1546)...(1584)
<223> Artificial spacer sequence

<221> misc_feature
<222> (1585)...(2973)
<223> K:trAPAO

<221> CDS
<222> (1)...(2973)

<221> misc_feature
<222> (1585)...(1587)
<223> Extra lysine

<400> 26
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
-20 -15 -10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc 96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
-5 1 5

gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
10 15 20

gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg 192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25 30 35 40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt 240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
45 50 55

ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc 288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
60 65 70

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg toa 336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
75 80 85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac gcc ggc 384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
90 95 100

ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg 432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala

105	110	115	120	
ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac				480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn				
125	130	135		
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc				528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr				
140	145	150		
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg				576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg				
155	160	165		
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc gcc cga gtg				624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val				
170	175	180		
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc				672
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu				
185	190	195	200	
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt				720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser				
205	210	215		
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg				768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser				
220	225	230		
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca				816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro				
235	240	245		
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac				864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp				
250	255	260		
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg				912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu				
265	270	275	280	
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt				960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val				
285	290	295		
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg				1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly				
300	305	310		
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg				1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala				
315	320	325		
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac				1104
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp				
330	335	340		
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc gcc gac aat				1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn				
345	350	355	360	

cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag	1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln	
365 370 375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly	
380 385 390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc	1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	
425 430 435 440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct	1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro	
445 450 455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc	1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	
460 465 470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc	1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	
475 480 485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc	1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	
490 495 500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	1632
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly	
505 510 515 520	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
525 530 535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
540 545 550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
555 560 565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
570 575 580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
585 590 595 600	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	

605	610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 620 625 630			1968
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 635 640 645			2016
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 650 655 660			2064
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 665 670 675 680			2112
ggg gtt gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 685 690 695			2160
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700 705 710			2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 715 720 725			2256
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 730 735 740			2304
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 745 750 755 760			2352
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 765 770 775			2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780 785 790			2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 795 800 805			2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 810 815 820			2544
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825 830 835 840			2592
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845 850 855			2640

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg 2688
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 860 865 870

 gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 2736
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 875 880 885

 ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa 2784
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 890 895 900

 gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 2832
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 905 910 915 920

 tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 2880
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 925 930 935

 acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 2928
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 940 945 950

 caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 2973
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 955 960 965

 tag 2976

<210> 27
 <211> 991
 <212> PRT
 <213> Unknown

 <220>
 <221> SIGNAL
 <222> (1)...(24)

<400> 27
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
 -20 -15 -10
 Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
 -5 1 5
 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
 10 15 20
 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
 25 30 35 40
 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
 45 50 55
 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
 60 65 70
 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
 75 80 85
 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
 90 95 100
 Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
 105 110 115 120
 Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
 125 130 135
 Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
 140 145 150

Gly	Thr	Ser	Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg
		155					160					165			
Trp	Val	Gln	Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val
		170					175					180			
Thr	Val	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu
185					190					195					200
Thr	Ser	Pro	Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser
				205					210					215	
Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser
			220					225					230		
Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro
		235					240					245			
Ala	Thr	Leu	Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp
		250				255					260				
Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu
265					270				275						280
Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val
				285					290					295	
Arg	Val	Leu	Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly
			300					305					310		
Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala
		315					320					325			
Gln	Phe	Gly	Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp
		330				335					340				
Gly	Arg	Ala	Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn
345					350				355						360
Gln	Phe	Asn	Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln
				365					370					375	
Gly	Ala	Pro	Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly
			380					385					390		
Arg	Ala	Pro	Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val
		395				400						405			
Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro
		410				415					420				
Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val
425					430				435						440
Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro
				445					450					455	
Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg
			460					465					470		
Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly
		475					480					485			
Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser
		490				495					500				
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
505					510					515					520
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
				525					530					535	
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
			540					545					550		
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
			555				560						565		
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
		570				575						580			
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
585					590				595						600
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
				605				610					615		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
			620					625					630		
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
			635				640						645		

```

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
650                      655                      660
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665                      670                      675                      680
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
685                      690                      695
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
700                      705                      710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
715                      720                      725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
730                      735                      740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                      750                      755                      760
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
765                      770                      775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
780                      785                      790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795                      800                      805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810                      815                      820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                      830                      835                      840
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
845                      850                      855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860                      865                      870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875                      880                      885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
890                      895                      900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                      910                      915                      920
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
925                      930                      935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
940                      945                      950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955                      960                      965

```

```

<210> 28
<211> 3618
<212> DNA
<213> Unknown

```

```

<220>
<223> gst:esp1:sp:K:trapao, 3618. 1-687, gst +
polylinker; 688-2190, esp1 mat; 2191-2226 spacer;
2227-3615, K:trAPAO, extra lysine; 3616-3618, stop
codon. For bacterial expression.

```

```

<221> CDS
<222> (1)...(3615)

<221> misc_feature
<222> (1)...(687)
<223> gast + polylinker

```

```

<221> mat_peptide
<222> (688)...(2190)
<223> esp1 mat

```

<221> misc_feature
 <222> (2191)...(2226)
 <223> spacer sequence

<221> misc_feature
 <222> (2227)...(3615)
 <223> K:trAPAO

<221> misc_feature
 <222> (2227)...(2229)
 <223> Extra lysine

<400> 28
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac 576
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg	720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	
225 230 235 240	
gtc ggc acg act act act gtc ccc ggc acc act gcg acc gtc agc gag	768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	
245 250 255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct	816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
260 265 270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt	864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	
275 280 285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctg cgt gag att	912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	
290 295 300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag	960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu	
305 310 315 320	
gac tgc ctg aac ctg aac atc tac gtc cca gga act gag aac aca aac	1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	
325 330 335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg	1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	
340 345 350	
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat	1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Asn Gln Asp	
355 360 365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct	1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
370 375 380	
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac	1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp	
385 390 395 400	
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc	1248
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly	
405 410 415	
ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga	1296
Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg	
420 425 430	
agt gtc gac gtc ctg ttg acg tct atg cca cac aac cca ccc ttc cga	1344
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg	

435				440				445				
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga	1392											
Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly												
450 455 460												
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc	1440											
Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr												
465 470 475 480												
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act	1488											
Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr												
485 490 495												
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg	1536											
Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu												
500 505 510												
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt	1584											
Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly												
515 520 525												
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga	1632											
Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly												
530 535 540												
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag	1680											
Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu												
545 550 555 560												
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat	1728											
Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr												
565 570 575												
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc	1776											
Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala												
580 585 590												
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag	1824											
Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln												
595 600 605												
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg	1872											
Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala												
610 615 620												
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc	1920											
Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser												
625 630 635 640												
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc	1968											
Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr												
645 650 655												
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc	2016											
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala												
660 665 670												
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat	2064											
Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn												
675 680 685												

gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690 695 700	2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720	2160
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly 725 730 735	2208
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val 740 745 750	2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765	2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780	2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800	2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815	2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830	2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly 835 840 845	2544
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 910	2736
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu 915 920 925	2784
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	2832

930	935	940	
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg			2880
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met			
945	950	955 960	
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg			2928
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val			
	965	970 975	
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt			2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys			
	980	985 990	
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg			3024
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val			
	995	1000 1005	
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct			3072
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro			
	1010	1015 1020	
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac			3120
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr			
	1025	1030 1035 1040	
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa			3168
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln			
	1045	1050 1055	
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc			3216
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala			
	1060	1065 1070	
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc			3264
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe			
	1075	1080 1085	
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta			3312
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val			
	1090	1095 1100	
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc			3360
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
	1105	1110 1115 1120	
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg			3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
	1125	1130 1135	
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac			3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
	1140	1145 1150	
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt			3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
	1155	1160 1165	
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa			3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
	1170	1175 1180	

ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg gct agc 3600
 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
 1185 1190 1195 1200

ctg gtg cca gca gca tag 3618
 Leu Val Pro Ala Ala
 1205

<210> 29
 <211> 1205
 <212> PRT
 <213> Unknown

<400> 29
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
 225 230 235 240
 Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
 245 250 255
 Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
 260 265 270
 Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
 275 280 285
 Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
 290 295 300
 Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu
 305 310 315 320
 Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
 325 330 335
 Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp
 340 345 350
 Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
 355 360 365
 Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro

370	375	380
Ala Ala Pro Gln Leu Pro	Ile Thr Gln Arg Asn	Leu Gly Phe Leu Asp
385	390	395
Gln Arg Phe Ala Leu Asp	Trp Val Gln Arg Asn	Ile Ala Ala Phe Gly
405	410	415
Gly Asp Pro Arg Lys Val	Thr Ile Phe Gly Gln	Ser Ala Gly Gly Arg
420	425	430
Ser Val Asp Val Leu Leu	Thr Ser Met Pro His	Asn Pro Pro Phe Arg
435	440	445
Ala Ala Ile Met Glu Ser	Gly Val Ala Asn Tyr	Asn Phe Pro Lys Gly
450	455	460
Asp Leu Ser Glu Pro Trp	Asn Thr Thr Val Gln	Ala Leu Asn Cys Thr
465	470	475
Thr Ser Ile Asp Ile Leu	Ser Cys Met Arg Arg	Val Asp Leu Ala Thr
485	490	495
Leu Met Asn Thr Ile Glu	Gln Leu Gly Leu Gly	Phe Glu Tyr Thr Leu
500	505	510
Asp Asn Val Thr Ala Val	Tyr Arg Ser Glu Thr	Ala Arg Thr Thr Gly
515	520	525
Asp Ile Ala Arg Val Pro	Val Leu Val Gly Thr	Val Ala Asn Asp Gly
530	535	540
Leu Leu Phe Val Leu Gly	Glu Asn Asp Thr Gln	Ala Tyr Leu Glu Glu
545	550	555
Ala Ile Pro Asn Gln Pro	Asp Leu Tyr Gln Thr	Leu Leu Gly Ala Tyr
565	570	575
Pro Ile Gly Ser Pro Gly	Ile Gly Ser Pro Gln	Asp Gln Ile Ala Ala
580	585	590
Ile Glu Thr Glu Val Arg	Phe Gln Cys Pro Ser	Ala Ile Val Ala Gln
595	600	605
Asp Ser Arg Asn Arg Gly	Ile Pro Ser Trp Arg	Tyr Tyr Asn Ala
610	615	620
Thr Phe Glu Asn Leu Glu	Leu Phe Pro Gly Ser	Glu Val Tyr His Ser
625	630	635
Ser Glu Val Gly Met Val	Phe Gly Thr Tyr Pro	Val Ala Ser Ala Thr
645	650	655
Ala Leu Glu Ala Gln Thr	Ser Lys Tyr Met Gln	Gly Ala Trp Ala Ala
660	665	670
Phe Ala Lys Asn Pro Met	Asn Gly Pro Gly Trp	Lys Gln Val Pro Asn
675	680	685
Val Ala Ala Leu Gly Ser	Pro Gly Lys Ala Ile	Gln Val Asp Val Ser
690	695	700
Pro Ala Thr Ile Asp Gln	Arg Cys Ala Leu Tyr	Thr Arg Tyr Tyr Thr
705	710	715
Glu Leu Gly Thr Ile Ala	Pro Arg Thr Phe Gly	Gly Gly Ser Gly Gly
725	730	735
Gly Ser Gly Gly Gly Ser	Lys Asp Asn Val Ala	Asp Val Val Val Val
740	745	750
Gly Ala Gly Leu Ser Gly	Leu Glu Thr Ala Arg	Lys Val Gln Ala Ala
755	760	765
Gly Leu Ser Cys Leu Val	Leu Glu Ala Met Asp	Arg Val Gly Gly Lys
770	775	780
Thr Leu Ser Val Gln Ser	Gly Pro Gly Arg Thr	Thr Thr Ile Asn Asp
785	790	795
Gly Ala Ala Trp Ile Asn	Asp Ser Asn Gln Ser	Glu Val Ser Arg Leu
805	810	815
Phe Glu Arg Phe His Leu	Glu Gly Glu Leu Gln	Arg Thr Thr Gly Asn
820	825	830
Ser Ile His Gln Ala Gln	Asp Gly Thr Thr Thr	Ala Pro Tyr Gly
835	840	845
Asp Ser Leu Leu Ser Glu	Glu Val Ala Ser Ala	Leu Ala Glu Leu Leu
850	855	860
Pro Val Trp Ser Gln Leu	Ile Glu Glu His Ser	Leu Gln Asp Leu Lys

```

865          870          875          880
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr
          885          890          895
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln
          900          905          910
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu
          915          920          925
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe
          930          935          940
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met
945          950          955          960
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val
          965          970          975
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
          980          985          990
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val
          995          1000          1005
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro
1010          1015          1020
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr
1025          1030          1035          1040
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln
          1045          1050          1055
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala
          1060          1065          1070
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe
          1075          1080          1085
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
1090          1095          1100
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
1105          1110          1115          1120
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
          1125          1130          1135
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
          1140          1145          1150
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
          1155          1160          1165
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
1170          1175          1180
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
1185          1190          1195          1200
Leu Val Pro Ala Ala
          1205

```

```

<210> 30
<211> 3591
<212> DNA
<213> Unknown

```

```

<220>
<223> Open reading frame of BEST1:K:trAPAO fusion for
bacterial expression vector pGEX-4T-1 or similar
vector.
gst:BST1:sp:K:trAPAO fusion, 3591 nt. 1-687 gst +
polylinker, 688-2163, BEST1 mature; 2164-2199,
spacer, 2200-3588, K:trAPAO

```

```

<221> misc_feature
<222> (1)...(687)
<223> gst + polylinker

<221> mat_peptide

```

<222> (688)...(2163)

<223> BEST1 mature

<221> misc_feature

<222> (2164)...(2199)

<223> spacer sequence

<221> misc_feature

<222> (2200)...(3588)

<223> K:trAPAO

<221> CDS

<222> (1)...(3588)

<221> misc_feature

<222> (2200)...(2202)

<223> Extra lysine

<400> 30

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
ggt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	

gtt Val	tgt Cys	ttt Phe	aaa Lys 180	aaa Lys	cgt Arg	att Ile	gaa Glu	gct Ala	atc Ile	cca Pro	caa Gln	att Ile	gat Asp 190	aag Lys	tac Tyr	576
ttg Leu	aaa Lys	tcc Ser 195	agc Ser	aag Lys	tat Tyr	ata Ile	gca Ala 200	tgg Trp	cct Pro	ttg Leu	cag Gln	ggc Gly 205	tgg Trp	caa Gln	gcc Ala	624
acg Thr	ttt Phe 210	ggt Gly	ggt Gly	ggc Gly	gac Asp	cat His 215	cct Pro	cca Pro	aaa Lys	tcg Ser	gat Asp 220	ctg Leu	gtt Val	ccg Pro	cgt Arg	672
gga Gly 225	tcc Ser	ccg Pro	gaa Glu	ttc Phe	acg Thr 230	gat Asp	ttt Phe	ccg Pro	gtc Val	cgc Arg 235	agg Arg	acc Thr	gat Asp	ctg Leu	ggc Gly 240	720
cag Gln	gtt Val	cag Gln	gga Gly	ctg Leu 245	gcc Ala	ggg Gly	gac Asp	gtg Val	atg Met 250	agc Ser	ttt Phe	cgc Arg	gga Gly	ata Ile 255	ccc Pro	768
tat Tyr	gca Ala	gcg Ala	ccg Pro 260	ccg Pro	gtg Val	ggc Gly	ggg Gly	ctg Leu 265	cgt Arg	tgg Trp	aag Lys	ccg Pro	ccc Pro 270	caa Gln	cac His	816
gcc Ala	cgg Arg	ccc Pro 275	tgg Trp	gcg Ala	ggc Gly	gtt Val	cgc Arg 280	ccc Pro	gcc Ala	acc Thr	caa Gln	ttt Phe 285	ggc Gly	tcc Ser	gac Asp	864
tgc Cys	ttc Phe 290	ggc Gly	gcg Ala	gcc Ala	tat Tyr	ctt Leu 295	cgc Arg	aaa Lys	ggc Gly	agc Ser	ctc Leu 300	gcc Ala	ccc Pro	ggc Gly	gtg Val	912
agc Ser 305	gag Glu	gac Asp	tgt Cys	ctt Leu 310	tac Tyr	ctc Leu	aac Asn	gta Val	tgg Trp	gcg Ala	ccg Pro	tca Ser	ggc Gly	gct Ala	aaa Lys 320	960
ccc Pro	ggc Gly	cag Gln	tac Tyr	ccc Pro 325	gtc Val	atg Met	gtc Val	tgg Trp	gtc Val 330	tac Tyr	ggc Gly	ggc Gly	ggc Gly	ttc Phe 335	gcc Ala	1008
ggc Gly	ggc Gly	acg Thr	gcc Ala 340	gcc Ala	atg Met	ccc Pro	tac Tyr	tac Tyr 345	gac Asp	ggc Gly	gag Glu	gcg Ala	ctt Leu 350	gcg Ala	cga Arg	1056
cag Gln	ggc Gly	gtc Val 355	gtc Val	gtg Val	gtg Val	acg Thr	ttt Phe 360	aac Asn	tat Tyr	cgg Arg	acg Thr	aac Asn 365	atc Ile	ctg Leu	ggc Gly	1104
ttt Phe	ttc Phe 370	gcc Ala	cat His	cct Pro	ggt Gly	ctc Leu 375	tcg Ser	cgc Arg	gag Glu	agc Ser	ccc Pro 380	acc Thr	gga Gly	act Thr	tcg Ser	1152
ggc Gly 385	aac Asn	tac Tyr	ggc Gly	cta Leu	ctc Leu 390	gac Asp	att Ile	ctc Leu	gcc Ala	gct Ala 395	ctt Leu	cgg Arg	tgg Trp	gtg Val	cag Gln 400	1200
agc Ser	aac Asn	gcc Ala	cgc Arg	gcc Ala 405	ttc Phe	gga Gly	ggg Gly	gac Asp	ccc Pro 410	ggc Gly	cga Arg	gtg Val	acg Thr	gtc Val	ttt Phe 415	1248
ggt	gaa	tcg	gcc	gga	gcg	agc	gcg	atc	gga	ctt	ctg	ctc	acc	tcg	ccg	1296

Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	Thr	Ser	Pro	
			420					425					430			
ctg	agc	aag	ggc	ctc	ttc	cgt	ggc	gct	atc	ctc	gaa	agt	cca	ggg	ctg	1344
Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	Pro	Gly	Leu	
		435					440					445				
acg	cga	ccg	ctc	gcg	acg	ctc	gcc	gac	agc	gcc	gcc	tcg	ggc	gag	cgc	1392
Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	Gly	Glu	Arg	
	450					455					460					
ctc	gac	gcc	gat	ctt	tcg	cga	ctg	cgc	tcg	acc	gac	cca	gcc	acc	ctg	1440
Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	Ala	Thr	Leu	
465					470					475					480	
atg	gcg	cgc	gcc	gac	gcg	gcc	cgc	ccg	gca	tcg	cgg	gac	ctg	cgc	agg	1488
Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	Leu	Arg	Arg	
				485					490					495		
ccg	cgt	ccg	acc	gga	ccg	atc	gtc	gat	ggc	cat	gtg	ctg	ccg	cag	acc	1536
Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr	
			500					505					510			
gac	agc	gcg	gcg	atc	gcg	gcg	ggg	cag	ctg	gcg	ccg	gtt	cgg	gtc	ctg	1584
Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu	
		515					520					525				
atc	gga	acc	aat	gcc	gac	gaa	ggc	cgc	gcc	ttc	ctc	ggg	cgc	gcg	ccg	1632
Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro	
	530					535					540					
atg	gag	acg	cca	gcg	gac	tac	caa	gcc	tat	ctg	gag	gcg	cag	ttt	ggc	1680
Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly	
545					550					555					560	
gac	caa	gcc	gcc	gcc	gtg	gcg	gcg	tgc	tat	ccc	ctc	gac	ggc	cgg	gcc	1728
Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala	
				565					570					575		
acg	ccc	aag	gaa	atg	gtc	gcg	cgc	atc	ttc	ggc	gac	aat	cag	ttc	aat	1776
Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn	
			580					585					590			
cgg	ggg	gtc	tcg	gcc	ttc	tcg	gaa	gcg	ctt	gtg	cgc	cag	ggc	gcg	ccc	1824
Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro	
		595					600					605				
gtg	tgg	cgt	tat	cag	ttc	aac	ggc	aat	acc	gag	ggc	gga	aga	gcg	ccg	1872
Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro	
	610					615					620					
gct	acc	cac	gga	gcc	gaa	att	ccc	tac	gtt	ttc	ggg	gtg	ttc	aag	ctc	1920
Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu	
625					630					635					640	
gac	gag	ttg	ggc	ctg	ttc	gat	tgg	ccg	ccc	gag	ggg	ccc	acg	ccc	gcc	1968
Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala	
				645					650					655		
gac	cgt	gcg	ctg	ggc	caa	ctg	atg	tcc	tcc	gcc	tgg	gtc	cgg	ttc	gcc	2016
Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala	
			660					665					670			

aag Lys	aat Asn	ggc Gly 675	gac Asp	ccc Pro	gcc Ala	ggg Gly	gac Asp 680	gcc Ala	ctt Leu	acc Thr	tgg Trp	cct Pro 685	gcc Ala	tat Tyr	tct Ser	2064
acg Thr	ggc Gly 690	aag Lys	tcg Ser	acc Thr	atg Met	aca Thr 695	ttc Phe	ggt Gly	ccc Pro	gag Glu	ggc Gly 700	cgc Arg	gcg Ala	gcg Ala	gtg Val	2112
gtg Val 705	tcg Ser	ccc Pro	gga Gly	cct Pro	tcc Ser 710	atc Ile	ccc Pro	cct Pro	tgc Cys	gcg Ala 715	gat Asp	ggc Gly	gcc Ala	aag Lys	gcg Ala 720	2160
ggg Gly	ggc Gly	gga Gly	ggc Gly	agc Ser 725	ggc Gly	gga Gly	ggc Gly	agc Ser	ggc Gly 730	gga Gly	ggc Gly	agc Ser	aaa Lys	gac Asp 735	aac Asn	2208
gtt Val	gcg Ala	gac Asp	gtg Val 740	gta Val	gtg Val	gtg Val	ggc Gly	gct Ala 745	ggc Gly	ttg Leu	agc Ser	ggg Gly 750	ttg Leu	gag Glu	acg Thr	2256
gca Ala	cgc Arg	aaa Lys 755	gtc Val	cag Gln	gcc Ala	gcc Ala	ggg Gly 760	ctg Leu	tcc Ser	tgc Cys	ctc Leu	ggt Val 765	ctt Leu	gag Glu	gcg Ala	2304
atg Met	gat Asp 770	cgt Arg	gta Val	ggg Gly	gga Gly	aag Lys 775	act Thr	ctg Leu	agc Ser	gta Val 780	caa Gln	tcg Ser	ggg Gly	ccc Pro	ggc Gly	2352
agg Arg 785	acg Thr	act Thr	atc Ile	aac Asn	gac Asp 790	ctc Leu	ggc Gly	gct Ala	gcg Ala 795	tgg Trp	atc Ile	aat Asn	gac Asp	agc Ser	aac Asn 800	2400
caa Gln	agc Ser	gaa Glu	gta Val 805	tcc Ser	aga Arg	ttg Leu	ttt Phe	gaa Glu 810	aga Arg	ttt Phe	cat His	ttg Leu	gag Glu	ggc Gly 815	gag Glu	2448
ctc Leu	cag Gln	agg Arg	acg Thr 820	act Thr	gga Gly	aat Asn	tca Ser	atc Ile 825	cat His	caa Gln	gca Ala	caa Gln 830	gac Asp	ggg Gly	aca Thr	2496
acc Thr	act Thr	aca Thr 835	gct Ala	cct Pro	tat Tyr	ggg Gly 840	gac Asp	tcc Ser	ttg Leu	ctg Leu	agc Ser 845	gag Glu	gag Glu	gtt Val	gca Ala	2544
agt Ser	gca Ala 850	ctt Leu	gcg Ala	gaa Glu	ctc Leu	ctc Leu 855	ccc Pro	gta Val	tgg Trp	tct Ser	cag Gln 860	ctg Leu	atc Ile	gaa Glu	gag Glu	2592
cat His 865	agc Ser	ctt Leu	caa Gln	gac Asp 870	ctc Leu	aag Lys	gcg Ala	agc Ser	cct Pro	cag Gln 875	gcg Ala	aag Lys	cgg Arg	ctc Leu 880	gac Asp	2640
agt Ser	gtg Val	agc Ser	ttc Phe 885	gcg Ala	cac His	tac Tyr	tgt Cys	gag Glu	aag Lys 890	gaa Glu	cta Leu	aac Asn	ttg Leu	cct Pro 895	gct Ala	2688
gtt Val	ctc Leu	ggc Gly 900	gta Val	gca Ala	aac Asn	cag Gln	atc Ile 905	aca Thr	cgc Arg	gct Ala	ctg Leu	ctc Leu 910	ggg Gly	gtg Val	gaa Glu	2736
gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aaq	aqg	qcc	2784

Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala		
		915					920					925					
acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat		2832
Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr		
	930					935					940						
atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag		2880
Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys		
	945				950					955					960		
gaa	ctt	ggt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att		2928
Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile		
				965					970					975			
gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg		2976
Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val		
			980					985					990				
ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc		3024
Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro		
		995					1000						1005				
acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg		3072
Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala		
	1010					1015					1020						
gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac		3120
Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp		
	1025				1030					1035					1040		
aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc		3168
Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser		
				1045					1050					1055			
tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga		3216
Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg		
			1060					1065					1070				
caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg		3264
Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp		
		1075					1080					1085					
tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc		3312
Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu		
	1090					1095					1100						
cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac		3360
Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn		
	1105				1110					1115				1120			
gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg		3408
Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro		
				1125				1130					1135				
agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	ctc		3456
Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu		
			1140					1145					1150				
aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta		3504
Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu		
		1155					1160					1165					

ggt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa cga ggt 3552
 Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
 1170 1175 1180

gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 3591
 Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 1185 1190 1195

<210> 31
 <211> 1196
 <212> PRT
 <213> Unknown

<400> 31
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
 225 230 235 240
 Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
 245 250 255
 Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
 260 265 270
 Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
 275 280 285
 Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
 290 295 300
 Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
 305 310 315 320
 Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
 325 330 335
 Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
 340 345 350
 Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly

Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	Gly	Thr	Ser	
	370					375					380					
Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	Trp	Val	Gln	
385					390					395					400	
Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	Thr	Val	Phe	
				405					410					415		
Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	Thr	Ser	Pro	
				420				425					430			
Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	Pro	Gly	Leu	
		435					440					445				
Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	Gly	Glu	Arg	
						455					460					
Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	Ala	Thr	Leu	
465					470						475				480	
Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	Leu	Arg	Arg	
				485						490				495		
Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr	
				500				505					510			
Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu	
		515					520					525				
Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro	
						535					540					
Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly	
545					550					555					560	
Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala	
				565						570				575		
Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn	
				580				585					590			
Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro	
		595					600					605				
Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro	
						615					620					
Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu	
625					630					635					640	
Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala	
				645						650				655		
Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala	
				660				665					670			
Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser	
		675					680					685				
Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	Ala	Ala	Val	
		690				695</										

```

      850              855              860
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
865              870              875              880
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
              885              890              895
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu
              900              905              910
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
              915              920              925
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
              930              935              940
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
945              950              955              960
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
              965              970              975
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
              980              985              990
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
              995              1000              1005
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala
              1010              1015              1020
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp
1025              1030              1035              1040
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser
              1045              1050              1055
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg
              1060              1065              1070
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
              1075              1080              1085
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu
              1090              1095              1100
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
1105              1110              1115              1120
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
              1125              1130              1135
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
              1140              1145              1150
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
              1155              1160              1165
Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
              1170              1175              1180
Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
1185              1190              1195

```

<210> 32

<211> 2490

<212> DNA

<213> Unknown

<220>

<223> GST:glyc(-)APAO open reading frame, 2490 nt; GST and linker, nt 1-687; Glyc (-) APAO, nt 688-2490; mutation in putative glycosylation sites in bold and underlined, nt 1288-1290 (AAT->TCC) and nt 1303-1305 (AGC->AAC).

<221> CDS

<222> (1)...(2487)

<221> misc_feature

<222> (1)...(687)

<223> GST and linker

<221> misc_feature
 <222> (688)...(2490)
 <223> Glyc (-) APAO

<221> mutation
 <222> (1288)...(1290)
 <223> mutation in putative glycosylation site (AAT->TCC)

<221> mutation
 <222> (1303)...(1305)
 <223> mutation in putative glycosylation site (AGC->AAC)

<400> 32
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac 576
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190

ttg	aaa	tcc	agc	aag	tat	ata	gca	tgg	cct	ttg	cag	ggc	tgg	caa	gcc	624
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
		195					200					205				
acg	ttt	ggg	ggg	ggc	gac	cat	cct	cca	aaa	tcg	gat	ctg	gtt	cgg	cgt	672
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
gga	tcc	cgg	gaa	ttc	atg	gca	ctt	gca	cgg	agc	tac	atc	aat	ccc	cca	720
Gly	Ser	Pro	Glu	Phe	Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	
225					230					235					240	
aac	gtc	gcc	tcc	cca	gca	ggg	tat	tct	cac	gtc	ggc	gta	ggc	cca	gac	768
Asn	Val	Ala	Ser	Pro	Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	
				245					250					255		
gga	ggg	agg	tat	gtg	aca	ata	gct	gga	cag	att	gga	caa	gac	gct	tcg	816
Gly	Gly	Arg	Tyr	Val	Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	
			260					265					270			
ggc	gtg	aca	gac	cct	gcc	tac	gag	aaa	cag	gtt	gcc	caa	gca	ttc	gcc	864
Gly	Val	Thr	Asp	Pro	Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	
		275					280					285				
aat	ctg	cga	gct	tgc	ctt	gct	gca	gtt	gga	gcc	act	tca	aac	gac	gtc	912
Asn	Leu	Arg	Ala	Cys	Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	
	290					295					300					
acc	aag	ctc	aat	tac	tac	atc	gtc	gac	tac	gcc	cgg	agc	aaa	ctc	acc	960
Thr	Lys	Leu	Asn	Tyr	Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	
305					310					315					320	
gca	att	gga	gat	ggg	ctg	aag	gct	acc	ttt	gcc	ctt	gac	agg	ctc	cct	1008
Ala	Ile	Gly	Asp	Gly	Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	
				325					330					335		
cct	tgc	acg	ctg	gtg	cca	gtg	tcg	gcc	ttg	tct	tca	cct	gaa	tac	ctc	1056
Pro	Cys	Thr	Leu	Val	Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	
			340					345					350			
ttt	gag	gtt	gat	gcc	acg	gcg	ctg	gtg	cgg	gga	cac	acg	acc	cca	gac	1104
Phe	Glu	Val	Asp	Ala	Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	
		355					360					365				
aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggg	ttg	gag	1152
Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	
	370					375					380					
acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggg	ctg	tcc	tgc	ctc	gtt	ctt	gag	1200
Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	
385					390					395					400	
gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggg	ccc	1248
Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	
				405					410					415		
ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	tcc	gac	agc	1296
Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Ser	Asp	Ser	
			420					425					430			
aac	caa	aac	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	1344
Asn	Gln	Asn	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	

435	440	445	
gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly 450 455 460			1392
aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val 465 470 475 480			1440
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu 485 490 495			1488
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu 500 505 510			1536
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro 515 520 525			1584
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val 530 535 540			1632
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser 545 550 555 560			1680
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln 565 570 575			1728
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser 580 585 590			1776
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu 595 600 605			1824
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala 610 615 620			1872
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr 625 630 635 640			1920
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 645 650 655			1968
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp 660 665 670			2016
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser 675 680 685			2064

agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	2112
Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	
690						695				700						
cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	2160
Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	
705					710					715					720	
tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	2208
Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	
				725					730					735		
ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	2256
Leu	Arg	Ala		Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	
			740				745						750			
aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	2304
Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	
	755						760					765				
ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	gcg	2352
Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	
	770					775					780					
ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	2400
Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	
	785				790					795					800	
tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggg	caa	cga	2448
Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	
				805					810					815		
ggg	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	tag			2490
Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala				
			820					825								

<210> 33
 <211> 829
 <212> PRT
 <213> Unknown

<400> 33

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5					10					15		
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
		20						25					30			
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35					40					45				
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50				55					60						
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
65				70					75					80		
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
			85					90					95			
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
		100						105					110			
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
		115					120					125				
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130					135					140					
Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	

145					150					155				160
Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys
				165						170				175
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys
			180										190	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln
		195					200					205		Ala
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro
	210					215					220			Arg
Gly	Ser	Pro	Glu	Phe	Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro
225					230					235				240
Asn	Val	Ala	Ser	Pro	Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro
				245					250					255
Gly	Gly	Arg	Tyr	Val	Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala
		260						265				270		Ser
Gly	Val	Thr	Asp	Pro	Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe
	275						280				285			Ala
Asn	Leu	Arg	Ala	Cys	Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp
	290				295						300			Val
Thr	Lys	Leu	Asn	Tyr	Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu
305				310					315					Thr
Ala	Ile	Gly	Asp	Gly	Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu
			325						330					Pro
Pro	Cys	Thr	Leu	Val	Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr
		340					345					350		Leu
Phe	Glu	Val	Asp	Ala	Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro
	355					360					365			Asp
Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu
	370				375					380				Glu
Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu
385				390					395					Glu
Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
			405					410						Pro
Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Ser	Asp
	420						425				430			Ser
Asn	Gln	Asn	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
	435					440					445			Gly
Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
450					455					460				Gly
Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
465				470					475					Val
Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile
			485					490					495	Glu
Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
	500						505				510			Leu
Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
	515					520					525			Pro
Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
	530				535					540				Val
Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
545				550					555					Ser
Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
			565					570					575	Gln
Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met
	580						585					590		Ser
Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala
	595					600					605			Glu
Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly
	610				615				620					Ala
Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu
625				630					635					Tyr
Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala
														Leu